

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:54 ; Search time 180.87 Seconds

(without alignments)  
38,818 Million cell updates/sec

Title: US-08-569-749-10

Perfect score: 294

Sequence: 1 PEQLASAGFYVGNSDVYKC.....CWESGDDPMVQHAKFPKCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	100.0	1140	4 Q9UNH1	Q9unh1 homo sapien
2	277	94.2	195	13 Q9IA70	Q9ia70 gallus gall
3	277	94.2	197	13 Q9IA69	Q9ia69 gallus gall
4	277	94.2	610	13 Q57319	Q57319 gallus gall
5	276	93.9	602	11 Q9ESES	Q9eses rattus norv
6	270	91.8	589	11 Q9QZC6	Q9qzc6 rattus norv
7	270	91.8	589	11 Q9ESES	Q9eses rattus norv
8	258	87.8	324	13 Q9DDN2	Q9ddn2 rattus norv
9	205	69.7	224	11 Q88642	Q88642 rattus norv
10	202	68.7	264	12 Q9EN27	Q9en27 amascta moe
11	193	65.6	281	12 Q9YNL8	Q9ynl8 homo sapien
12	193	65.6	281	12 Q9YNL8	Q9ynl8 choristoneu
13	193	65.6	298	4 Q9H2A8	Q9h2a8 homo sapien
14	191	65.0	276	12 Q89744	Q89744 buzzara supp
15	191	65.0	379	5 Q9U492	Q9u492 trichoplusi
16	190	64.6	379	5 Q9U492	Q9u492 trichoplusi
17	180	61.2	597	11 Q9H015	Q9h015 mus musculu
18	177	60.2	496	11 Q9E5F0	Q9e5f0 rattus norv
19	177	60.2	501	11 Q9E505	Q9e505 rattus norv

20	177	60.2	501	11 Q9E504	Q9e504 rattus norv
21	173	58.8	313	12 Q9J827	Q9j827 spodoptera
22	169	57.5	261	12 Q9E859	Q9e859 epiphyas po
23	163	55.4	438	5 Q9VUX5	Q9vux5 drosophila
24	125	42.5	268	12 Q9E232	Q9e232 helioverpa
25	125	42.5	268	12 Q9E232	Q9e232 helioverpa
26	123.5	42.0	4904	5 Q9VH01	Q9vh01 drosophila
27	122.5	41.7	153	5 Q9EWM2	Q9ewm2 drosophila
28	116.5	39.6	4845	11 Q88738	Q88738 mus musculu
29	115	39.5	150	12 Q9YVJ4	Q9yvJ4 melanoplus
30	111	37.8	292	12 Q92394	Q92394 bombyx mori
31	107	36.4	208	12 Q55770	Q55770 chilo fride
32	102.5	34.9	301	12 Q9P254	Q9p254 trichoplusi
33	102	34.7	284	12 Q9YKLS	Q9ykls epiphyas po
34	93	31.6	155	12 Q9YMI9	Q9ymi9 lymantria d
35	92.5	31.5	142	13 Q9DDK0	Q9ddk0 gallus gall
36	92.5	31.5	285	12 Q9PYQ9	Q9pyq9 xestia c-ni
37	86.5	29.4	142	6 Q9GLN5	Q9glN5 sus scrofa
38	81.5	27.7	187	12 Q9DSM8	Q9dsm8 ascovirus d
39	80	27.2	308	5 Q18727	Q18727 caenorhabdi
40	77	26.2	87	11 Q09119	Q09119 mus musculu
41	76	25.9	87	11 Q09120	Q09120 mus musculu
42	76	25.9	137	4 Q9B424	Q9b424 homo sapien
43	76	25.9	155	5 Q22837	Q22837 caenorhabdi
44	75	25.5	87	11 Q09123	Q09123 mus musculu
45	75	25.5	281	12 Q9DVT5	Q9dvt5 pluteia xy

## ALIGNMENTS

RESULT	ID	Q9UNH1	PRELIMINARY:	PRT:	1140 AA.
AC	Q9UNH1				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	API2-MUT FUSION PROTEIN.				
GN	API2-MUT.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Plimates; Carnivora; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE:9272400; PubMed:10339464;				
RA	Dierlam J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,				
RA	Hernandez J.M., Hossfeld D.K., De Wolf-Peters C., Hagemeijer A.,				
RA	Van den Bergh H., Marynen P.;				
RT	*The apoptosis inhibitor gene API2 and a novel 18q gene, MIT, are				
RT	recurrently rearranged in the t(11;18)(q21;q21)possociated with				
RT	mucosa-associated lymphoid tissue lymphomas.";				
RL	Blood 93;3:601-3609(1999).				
CC	-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX				
CC	DOMAIN.				
CC	EMBL: AF123094; AAD46161.1; -				
DR	HSSP: Q13490; IOBH.				
DR	InterPro: IPR001370; BIR.				
DR	InterPro: IPR003576; Caspase.				
DR	InterPro: IPR001308; ICE_P20.				
DR	InterPro: IPR003586; I9_C2.				
DR	InterPro: IPR003600; I9_Like.				
DR	InterPro: IPR003006; I9_MHC.				
DR	Pfam: PF00653; BIR; 3.				
DR	Pfam: PF00047; I9; 2.				
DR	SMART: SM00238; BIR; 3.				
DR	SMART: SM00115; CASC; 1.				
DR	SMART: SM00408; IGC2; 1.				
DR	SMART: SM00410; IC_Like; 1.				
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.				
DR	PROSITE: PS0143; BIR_REPEAT_2; 3.				
DR	PROSITE: PS0208; CASPASE_P20; 1.				



FT REPEAT 262 329 BIR REPEAT 3.  
 FT\_ZN\_FING 563 597 C3HC4-TYPE.  
 SQ SEQUENCE 610 AA; 68924 MW; ADF47619650844A6 CRC64;

Query Match 94.2%; Score 277; DB 13; Length 610;  
 Best Local Similarity 89.6%; Pred. No. 2, 9e-28;  
 Matches 43; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 48  
 ||||| ||||| :||||| ||||| ||||| ||||| :||||| |||||  
 Db 280 PEOIADAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 327

RESULT 5  
 ID Q9ESE9 PRELIMINARY; PRT; 602 AA.  
 AC Q9ESE9;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
 RT Apoptosis Protein 1, 2, and 3 Genes."  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL:AF183430; AAG22970.1; -;  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; ZnF\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR ZINC-finger.  
 SQ SEQUENCE 602 AA; 67326 MW; CC91385EEA62DE5A CRC64;

Query Match 93.9%; Score 276; DB 11; Length 602;  
 Best Local Similarity 89.6%; Pred. No. 3, 9e-28;  
 Matches 43; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 48  
 ||||| ||||| :||||| ||||| ||||| ||||| :||||| |||||  
 Db 273 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 320

RESULT 6  
 ID Q9QZC6 PRELIMINARY; PRT; 589 AA.  
 AC Q9QZC6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;  
 RA Dong Z., Denton M., Gu S.M., Saitkumar P., Venkatasalam M.A.;  
 RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL:AF190020; AAF04585.1; -;  
 DR HSSP: Q13490; IOBH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; ZnF\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR ZINC-finger.  
 SQ SEQUENCE 589 AA; 66777 MW; B6812FEE3EA34142 CRC64;

Query Match 91.8%; Score 270; DB 11; Length 589;  
 Best Local Similarity 87.5%; Pred. No. 2, 4e-27;  
 Matches 42; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 48  
 ||||| ||||| :||||| ||||| ||||| ||||| :||||| |||||  
 Db 259 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 306

RESULT 7  
 ID Q9SEB8 PRELIMINARY; PRT; 589 AA.  
 AC Q9SEB8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN 2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
 RT Apoptosis Protein 1, 2, and 3 Genes."  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL:AF183431; AAG22971.1; -;  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR001841; ZnF\_fing.  
 DR Pfam: PF00653; BIR; 3.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00238; BIR; 3.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 1.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE: PS50209; CARD; 1.  
 DR ZINC-finger.  
 SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;

Query Match 91.8%; Score 270; DB 11; Length 589;  
 Best Local Similarity 87.5%; Pred. No. 2, 4e-27;  
 Matches 42; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PEOIASAGFYVYVNSDDVYKCFCCDGLRCWESGDDPWVQHAKEPCE 48

Db 259 PEOLASAGFYVDHNDVCKFCDDGGLRCWEGDDPWVIAHAKMPRCE 306

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RESULT 8
Q9DDN2 PRELIMINARY: PRT: 324 AA.
ID Q9DDN2;
AC Q9DDN2;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE APOPTOSIS INHIBITOR CH-1AP1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RX [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;
RT "The Apoptosis Inhibitor ch-1ap1 is a direct transcriptional target of
v-Rel and c-Rel."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF11289; AAC42316.1; -.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR: 3.
DR SMART: SM00238; BIR: 3.
DR PROSITE: PS01282; BIR_REPEAT_1: 1.
DR PROSITE: PS0143; BIR_REPEAT_2: 3.
DR NON_TER 324 324
SQ SEQUENCE 324 AA: 36567 MW: 56289DEAE3733F3 CRC64;

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Query Match 87.8%; Score 258; DB 13; Length 324;  
 Best Local Similarity 88.9%; Pred. No. 4.8e-26;  
 Matches 40; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 PEOLASAGFYVGNSDVCKFCDDGGLRCWEGDDPWVIAHAKMPR 45  
 Db 280 PEOLADAGFYVGNNDVCKFCDDGGLRCWEGDDPWVIAHAKMPR 324

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RESULT 9
ID O88642 PRELIMINARY: PRT: 224 AA.
AC O88642;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-MISTAR; TISSUE-OVARY; CORPUS LUTEUM;
RA Bradley C.K., Careu R.R., Dharmarajan A.M.;
RT "Cloning and characterisation of an inhibitor of apoptosis protein
(RIAP) in the rat corpus luteum."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081503; AAC32497.1; -.
DR HSSP: Q13490; 108H.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR: 2.
DR SMART: SM00238; BIR: 2.
DR PROSITE: PS0143; BIR_REPEAT_2: 3.
DR NON_TER 1 1
SQ SEQUENCE 224 AA: 25209 MW: 213A52534D5EB56A CRC64;

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Query Match 69.7%; Score 205; DB 11; Length 224;  
 Best Local Similarity 89.2%; Pred. No. 3.1e-19;  
 Matches 33; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 PEOLASAGFYVGNSDVCKFCDDGGLRCWEGDDPW 37  
 Db 188 PEOLASAGFYVDHNDVCKFCDDGGLRCWEGDDPW 224

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RESULT 10
Q9EN27 PRELIMINARY: PRT: 264 AA.
ID Q9EN27;
AC Q9EN27;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE AMV021.
GN AMV021.
OS Amsacta moorei entomopoxvirus (AmpPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20396580; PubMed-10936094;
RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,
RT Moyer R.W.;
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
Analysis and Comparison with Other Poxviruses."
RT Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF250284; AAC02727.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_r1ng.
DR Pfam: PF00653; BIR: 2.
DR SMART: SM00238; BIR: 2.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS0143; BIR_REPEAT_2: 2.
SQ SEQUENCE 264 AA: 30547 MW: 2E872DA4B58D920A CRC64;

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Query Match 68.7%; Score 202; DB 12; Length 264;  
 Best Local Similarity 66.0%; Pred. No. 9e-19;  
 Matches 31; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 2 EOLASAGFYVGNSDVCKFCDDGGLRCWEGDDPWVIAHAKMPRCE 48  
 Db 126 EKLAEAGFYTGKSDVCKFCYCDGGLKRWETDDPWIOHAKWFDKDC 172

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RESULT 11
Q9HAP7 PRELIMINARY: PRT: 280 AA.
ID Q9HAP7;
AC Q9HAP7;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE LIVIN INHIBITOR OF APOPTOSIS (INHIBITOR OF APOPTOSIS) (BA261N1.1.1)
DE (BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 7 (LIVIN), ISOFORM 1).
GN LIVIN OR BIRC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Kasof G.M., Gomes B.C.;
RT "Livin, a novel inhibitor-of-apoptosis (IAP) family member."
RL J. Biol. Chem. 0:0-0(2000).

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RN [2]
RP SEQUENCE FROM N.A.
RA Ashab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
   different biological properties and tissue distribution pattern.";
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF311388; AAC33622.1; -.
DR EMBL: AJ309298; CAC37337.1; -.
DR EMBL: AL121827; CAC36112.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 1.
DR SMART: SM00238; BIR; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
KM Zinc-finger.
SO SEQUENCE 280 AA; 30866 MW; 630BE9C0737F7952 CRC64;

Query Match 65.6%; Score 193; DB 4; Length 280;
Best Local Similarity 60.4%; Pred. No. 1.5e-17;
Matches 29; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYVNSDDVKCFCCDGLRCWESGDDPVVQHAKEFPCE 48
DB 105 PELLAAGFHTGHODKRCFCYCGLOSKMRGDDPVTETAKKFPSCQ 152

RESULT 12
Q9YNL8 PRELIMINARY; PRT; 281 AA.
AC Q9YNL8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE IAP PROTEIN.
GN IAP.
OS Choristoneura fumiferana nuclear polyhedrosis virus (CFMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=10448;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-IRELAND;
RA Lauzon H., Atif B.M., Ladd T., Palli R.;
RT "CFMNPV IAP gene.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: U82510; AAC00537.1; -.
DR HSP: O13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE: PS50143; BIR_REPEAT_2; 2.
KM Zinc-finger.
SO SEQUENCE 281 AA; 32090 MW; B2D9E8A359F105E CRC64;

Query Match 65.6%; Score 193; DB 12; Length 281;
Best Local Similarity 68.1%; Pred. No. 1.5e-17;
Matches 32; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

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QY 1 PQLASAGFYVYVNSDDVKCFCCDGLRCWESGDDPVVQHAKEFPCE 47
DB 142 PEKLAAGFYVYVNSDDVKCFCCDGLRCWESGDDPVVQHAKEFPCE 188

RESULT 13
Q9H2A8 PRELIMINARY; PRT; 298 AA.
AC Q9H2A8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN KIAA (BA261N11.1.2) (BACULOVIRAL IAP
   REPEAT-CONTAINING PROTEIN 7 (LIVIN), ISORFORM 2).
GN BIRC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY.
RC lin J.-H., Deng G., Huang Q., Morser J.;
RT "A Novel member of the inhibitor of apoptosis protein family.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ashab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
   different biological properties and tissue distribution pattern.";
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hall R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF301009; AAC37878.1; -.
DR EMBL: AJ309298; CAC37338.1; -.
DR EMBL: AL121827; CAC36111.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
KM Zinc-finger.
SO SEQUENCE 298 AA; 32798 MW; B2EAAE531BEC101 CRC64;

Query Match 65.6%; Score 193; DB 4; Length 298;
Best Local Similarity 60.4%; Pred. No. 1.5e-17;
Matches 29; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 PQLASAGFYVYVNSDDVKCFCCDGLRCWESGDDPVVQHAKEFPCE 48
DB 105 PELLAAGFHTGHODKRCFCYCGLOSKMRGDDPVTETAKKFPSCQ 152

RESULT 14
O89744 PRELIMINARY; PRT; 276 AA.
AC O89744;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE APOPTOSIS INHIBITOR IAP-1.
GN IAP1.
OS Buzaia suppressaria nuclear polyhedrosis virus (BSNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=74320;

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